Amendments to the Specification

A. Please substitute the following paragraph in response to the Examiner's objection to the disclosure for containing an embedded hyperlink on Page 10.

Please replace the paragraph starting page 10, line 3, with the following paragraph.

a1

FIG. 14. Chromosomal localization of the mouse Npm2 gene. (Top) Map figure from the T31 radiation hybrid database at The Jackson Laboratory showing Chromosome 14 data. The map is depicted with the centromere toward the top. Distances between adjacent loci in centiRay3000 are shown to the left of the chromosome bar. The positions of some of the chromosome 14 MIT markers are shown on the right. *Npm2* is positioned between D14Mit203 and D14Mit32. Missing typings were inferred from surrounding data where assignment was unambiguous. Raw data were obtained from the ~~The Jackson Laboratory were obtained from the Wold Wide Web address http://www.jax.org/resources/documents /cmdata/rhmap/rh.html. (Bottom) Haplotype figure from the~~ T31 mouse radiation hybrid database from ~~at~~ The Jackson Laboratory (Bar Harbor, Maine) showing part of Chromosome 14 with loci linked to *Npm2*. Loci are listed in the best fit order with the most proximal at the top. The black boxes represent hybrid cell lines scoring positive for the mouse fragment and the white boxes represent cell lines scoring as negative. The grey box indicates an untyped or ambiguous line. The number of lines with each haplotype is given at the bottom of each column of boxes. Missing typings were inferred from surrounding data where assignment was unambiguous.

B. Please substitute the following paragraphs in response to the Examiner's objection to the disclosure on pages 12, 33, 43 and 45 for containing sequences not identified by a (SEQ ID NO).

Please replace the paragraph starting on page 12, line 24, with the following paragraph.

a2

FIG. 22A and 22B. Comparison of Oo1 gene and Oo1 pseudogene. Sequences of exons, exon-intron boundaries and the size of each intron are shown. Different nucleotides between the two genes and consensus polyadenylation sequence are underlined. The translation start codon and stop codon are shown in bold. The consensus donor sequence in

rodents is (SEQ ID NO:26) (C/A)AG/GTURAGT and the consensus acceptor sequence is (SEQ ID NO:27) YYYYYYYYYYNCAG/G (Y, pyrimidine; RU, purine; N, any nucleotide) (Senapathy et al., 1990). Upper case: exon sequences; lower case: intron sequences

Please replace the paragraph starting on page 33, line 15, with the following paragraph.

To map the mouse *Npm2* gene, we used the Research Genetics radiation hybrid panel, The Jackson Laboratory Backcross DNA Panel Mapping Resource, and The Jackson Laboratory Mouse Radiation Hybrid Database. Forward (SEQ ID NO:28) (GCAAAGAAGC CAGTGACCAA GAAATGA) and reverse (SEQ ID NO:29) (CCTGATCATG CAAATTTTAT TGTGGCC) primers within the last exon were used to PCR amplify a 229 bp fragment from mouse but not hamster. Using these primers, the mouse *Npm2* gene was mapped to the middle of chromosome 14 (Figure 14). *Npm2* shows linkage to D14Mit32 with a LOD of 11.2 and also has a LOD of 7.8 to D14Mit203. This region is syntenic with human chromosome 8p21.

Please replace the paragraph starting on page 43 , line 19 and finishing on page 44, line 4, with the following paragraph.

The whole genome-radiation hybrid panel T31 (McCarthy et al., 1997) were purchased from Research Genetics (Huntsville, AL) and used according to the manufacturer's instruction. The panel was constructed by fusing irradiated mouse embryo primary cells (129aa) with hamster cells. Because the sequence of the hamster homologues for Oo1 is unknown, the inventors designed the reverse primers from the 3'-untranslated region of the murine sequence to minimize the risk of coamplification of the hamster homologues (Makalowski and Boguski, 1998). Oo1 gene specific primers were (SEQ ID NO:30) 5'-CTAGAAAAGGGGACTGTAGTCACT-3' forward, and (SEQ ID NO:31) 5'-TGCATCTCCCACACAAGTCTTGCC-3' reverse; pseudo Oo1 gene specific primers were (SEQ ID NO:32) 5'-CTAGAAAAGGGGACTATAGGCACC-3' forward, and (SEQ ID NO:33) 5'-TGCATCTCTCACACAAGTGTTGCT-3' reverse. Specificity of the two sets of primers was tested with A23 hamster DNA and 129 mouse DNA. The PCR reactions were performed in 15µl final volume, containing 1µl of each panel DNA, 1.25u of Taq platinum DNA polymerase (Gibco, Rockville, MD), companion reagents (0.25mM dNTPs, 1.5mM $MgCl_2$, 1xPCR buffer), and 0.4µM of each primer. An initial denaturation step of 4 min at

94°C was followed by amplification for 30 cycles (40s at 94°C, 30s at 60°C, and 30s at 72°C) and final elongation at 72°C for 7min.

a4

Please replace the paragraph starting on page 44 , line 25 and finishing on page 45, line 2, with the following paragraph.

a5

A ZAP-express mouse ovary cDNA library was screened to isolate the full-length Oo1 cDNA. Excluding the polyA tail, the full-length Oo1 cDNA is about 1.3kb, and encodes an open reading frame from nucleotides 26 to 1108. The Oo1 cDNA is homologous to several ESTs in the database, including ESTs in a mouse sixteen-cell embryo cDNA library (AU044294) and a mouse unfertilized egg cDNA library (AU023153). The polypeptide predicted from the Oo1 cDNA ORF consists of 361 amino acids, with a molecular mass of 40 kDa. Searching the public protein database failed to identify any known protein homologues. A bipartite nuclear localization signal was found at positions 333 to 350 (SEQ ID NO:34) (Lys-Arg-Pro-His-Arg-Gln-Asp-Leu-Cys-Gly-Arg-Cys-Lys-Asp-Lys-Arg-Leu-Ser), strongly suggesting that Oo1 is located in the oocyte nucleus.